

<!--StartFragment-->RESULT 5  
ABB75752  
ID ABB75752 standard; protein; 708 AA.  
XX  
AC ABB75752;  
XX  
DT 15-JUN-2007 (revised)  
DT 24-JUN-2002 (first entry)  
XX  
DE Human gp354 (putative splice variant).  
XX  
KW Human; GP354; immunoglobulin; pancreas; central nervous system;  
KW diagnosis; gene therapy; pancreatitis; inflammation; tumour; cancer;  
KW autoimmune disease; Alzheimer's disease; Parkinson's disease;  
KW senile dementia; migraine; epilepsy; neurasthenia; neuropathy;  
KW neural degeneration; antiinflammatory; cytostatic; nootropic;  
KW immunosuppressive; antiparkinsonian; neuroprotective; antimigraine;  
KW anticonvulsant; splice variant; BOND\_PC; LRMR5827;  
KW LRMR5827 [Homo sapiens]; GO7155; GO16020; GO16021.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .21  
FT /label= Signal\_peptide  
FT Protein 22. .708  
FT /label= Mature\_protein  
FT Domain 22. .510  
FT /note= "extracellular domain"  
FT Domain 38. .109  
FT /note= "Ig domain"  
FT Domain 139. .206  
FT /note= "Ig domain"  
FT Domain 242. .293  
FT /note= "Ig domain"  
FT Domain 326. .377  
FT /note= "Ig domain"  
FT Domain 413. .488  
FT /note= "Ig domain"  
FT Domain 511. .533  
FT /note= "transmembrane domain"  
FT Domain 534. .708  
FT /note= "intracellular domain"  
XX  
PN WO200198360-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US019904.  
XX  
PR 22-JUN-2000; 2000US-0213611P.  
XX  
PA (BIOJ ) BIOGEN INC.  
PA (CARU/) CARULLI J P.  
PA (LUKA/) LUKASHIN A V.  
PA (KILB/) KILBURN D R.  
PA (SUNC/) SUN C.  
XX  
PI Carulli JP, Lukashin AV, Kilburn DR, Sun C;  
XX  
DR WPI; 2002-329171/36.

DR N-PSDB; ABL53876.  
 DR PC:NCBI; gi55735519.  
 DR PC:SWISSPROT; Q6UWL6.  
 XX  
 PT Novel nucleic acid sequence encoding a member of immunoglobulin  
 PT superfamily, designated GP354, useful for the treatment of Alzheimer's  
 PT disease, Parkinson's disease, senile dementia, migraine and epilepsy.  
 XX  
 PS Claim 17; Fig 7; 163pp; English.  
 XX  
 CC The present sequence is that of human GP354 (see ABB75752), a novel  
 CC member of the immunoglobulin superfamily. The sequence is deduced from  
 CC gp354 cDNA (see ABL53876), but differs from the gene-derived protein  
 CC sequence (see ABB75751), e.g. at amino acid positions 195, 196, 539 and  
 CC 540, suggesting allelic variation or alternative splicing. GP354 is a  
 CC pancreas-enriched integral membrane protein, also detected at low levels  
 CC in the central nervous system (CNS). Its protein structure and tissue  
 CC distribution indicate a role in cell-cell recognition, binding,  
 CC signalling and adhesion events in the pancreas and CNS. The invention  
 CC provides GP354 polypeptides and gp354 polynucleotides, as well as  
 CC vectors, host cells, antibodies and related diagnostic and therapeutic  
 CC methods. Claimed compositions comprising a gp354 nucleic acid or GP354  
 CC polypeptide are used in the treatment of pancreatic injury and abnormal  
 CC or disease conditions that relate to the pancreas, such as acute or  
 CC chronic pancreatitis, pancreatic inflammation, pancreatic necrosis,  
 CC exocrine insufficiency, pancreatic endocrine and hormonal imbalance,  
 CC pancreatic tumours and associated cancers, and autoimmune disorders which  
 CC affect the pancreas. They are also used in the treatment of an injury to  
 CC the CNS and abnormal or disease conditions that relate to the CNS,  
 CC including Alzheimer's disease, Parkinson's disease, senile dementia,  
 CC migraine, epilepsy, neuritis, neurasthenia, neuropathy, neural  
 CC degeneration and neural tumours (all claimed)  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.  
 XX  
 SQ Sequence 708 AA;

Query Match 85.6%; Score 3156.5; DB 5; Length 708;  
 Best Local Similarity 84.3%; Pred. No. 2.7e-212;  
 Matches 594; Conservative 40; Mismatches 66; Indels 5; Gaps 2;

Qy	1	MLASALLVFLCCFKGHAGSSPHFLQQPEDMVVLGEEARLPCALGAYRGLVQWTKDGLAL	60
		::              :	
Db	4	MRVPALLVLLFCFRGRAGSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLAL	63

Qy	61	GGERDLPGWSRYWISGNSASGQHDLHIKPVELEDEASYECQASQAGLRSRPAQLHVMVPP	120
	:           :  :     :                 :         :		
Db	64	GGQRDLPGWSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPP	123

Qy	121	EAPQVLGGPSVSLVAGVPGNLTCRSRGDSRPAPELLWF RDGIRLDASSFHQTTLKDKATG	180
	:       :    :       :		
Db	124	EAPQVLGGPSVSLVAGV PANLTCSRSGDARPTPELLWF RDGVLLDGATFHQTLLKEGTPG	183

Qy	181	TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGER	240
	:  :               :               :		
Db	184	SVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTL SASPHTVQEGER	243

Qy	241	VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADATFLTEPVSC EVSNAVGSANRS	300
	:		
Db	244	VIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADASFLTEPVSC EVSNAVGSANRS	303

Qy	301 TALEVLYGPILQAKPKSVSDVGKDASFSCVWRGNPLPRITWTRMGGSQVLSSGPTLRLP 360    :   :       :               :        :
Db	304 TALDVLFGPILQAKPEPVSDVGEDASFSCAWRGNPLPRVTWTRRGGAQVLGSGATLRLP 363
Qy	361 SVALEDAGDYVCRAEPRRTGLGGGKAQARLTVNAPPVTALQPAPAFLRGPARLQCVVFA 420               :       :               :
Db	364 SVGPEDAGDYVCRAEAGLSQLRGAAEARLTVNAPPVTALHSAPAFLRGPARLQCLVFA 423
Qy	421 SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF 480      :                                 :
Db	424 SPAPDAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGLISVLHISGTQESDFSRSF 483
Qy	481 NCSARNRLGEGRVQIHLGRDPLLPTVRIVAGAASAATSLLMVITGVVLCCWRH---GSL 536                    :   :
Db	484 NCSARNRLGEGBAQASLGRRDPLLPTVRIVAGVAAATTLLMVITGVALCCWRHSKASF 543
Qy	537 SKQKNLVRIPGSSEGSSSRGP--EEETGSSEDRGPIVHTDHSDLVLEEKAELETKDPTNGY 595  :    :                           :
Db	544 SEQKNLMRIPGSSDGSSSRGPEEEETGSREDRGPIVHTDHSDLVLEEGTLETKDPTNGY 603
Qy	596 YKVRGVSVSLSLGEAPGGGLFLPPPSPIGLPGTPYYDFKPHLDLVPPCRLYRARAGYL 655              :   :    :        :
Db	604 YKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPFYDFNPHGMVPPCRLYRARAGYL 663
Qy	656 TPHRAFTSYMKP TSFGPPDLSSGT PFPYATLSPPSHQRLQTHV 700        :   :   :   :
Db	664 TPHRAFTSYIKPTSF GPPDLAPGT PFPYAAFPTPSHPRLQTHV 708

&lt;!--EndFragment--&gt;